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REMARKS/ARGUMENTS

Applicants have amended page 14 of the Specification to address the Examiner's objections to the specification.

Applicants have amended Claims 1, 2, 4, 17, 18 and 20-22 to more particularly claim the invention. Applicants submit that these amendments do not represent new matter because support for the same may be found in the specification and the originally submitted claims.

A. Objections to the Specification

The Examiner has objected to the Specification because it contains embedded hyperlink and/or other form of browser-executable code. Applicants have amended page 14, line 14 of the Specification to delete embedded hyperlink and/or other form of browser-executable code, thereby obviating this objection.

B. Rejection under 35 U.S.C. § 101 is obviated

Claims 1-8 have been rejected under 35 U.S.C. §101 as directed to a non-statutory subject matter. The Office Action asserts that the claims are not concrete as one would not know what characteristic of a biological sequence was being determined.

Applicants respectfully disagree as understanding the characteristics of a biological sequence is concrete, tangible and useful for many fields where sequence analysis is needed. However, for the purpose of expediting the issuance of claims, Applicants have amended Claim 1 to recite method and system for the determination of the orientation of a biological sequence. Support of the amendment may be found on Page 19 to Page 25 of the Specification. Applicants submit that no new matter is entered

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by the amendment. Applicants believe that this amendment obviate this rejection as the process for analyzing the sequence orientation produces a concrete, tangible and useful result. Therefore, Applicants respectfully submits that this rejection of Claims under 35 U.S.C § 101 is obviated by the amendment.

C. Rejection under 35 U.S.C § 112 second paragraph should be withdrawn.

Claims 1-8 and 17-24 are rejected under 35 U.S.C. § 112, second paragraph, as being indefinite.

Specifically, the Examiner alleges that it is not clear what characteristic is intended in Claims 1 and 17. Applicants respectfully disagree. However, for the purpose of expediting the issuance of claims, Applicants have amended Claim 1 and 17 to recite "orientation of a biological sequence" and "a biological sequence's orientation". Support of the amendments may be found on Page 19 to Page 25 of the Specification. Because the amended claims specifically recite a particular characteristic, Applicants respectfully submit that this rejection of Claims is obviated.

Claims 1 and 17 are rejected for allegedly being vague and indefinite for failing to point out what kind of evidence other than sequence annotation is being obtained. Applicants respectfully disagree. The rejected claims are directed to a process of analyzing sequence orientation using evidence about sequence orientation. It would be apparent to one of skill in the art what constitute evidence that may be used for the determination of sequence orientation. Therefore, this rejection of Claims should be withdrawn.

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Claims 2 and 18 are rejected for allegedly reciting "defining the prior probability of the biological sequence" without sufficient antecedent basis for "the prior probability". Applicants have amended Claims 2 and 18 to recite "*a* prior probability". Applicants respectfully that this rejection is obviated.

Claims 2 and 18 are rejected for allegedly reciting "evidence assuming the hypothesis is true" without sufficient antecedent basis for "the hypothesis". Applicants have amended Claims 2 and 18. Support for these amendments may be found in Figure 4 and in Page 19, line 15 to Page 21, line 12 of the Specification. Applicants respectfully submit that not new matter is entered by these amendments and respectfully submit that the rejection of Claims 2 and 18 is obviated by the amendment.

In summary, in view of the above amendments and arguments, Applicants respectfully submit that this rejection of Claims 1-8 and 17-24 under 35 U.S.C. 112, second paragraph, should be withdrawn.

D. Rejection under 35 U.S.C. § 102 should be withdrawn

Claims 1-3 and 17-19 are rejected under 35 U.S.C. § 102(b) as being anticipated by Ma et al. (1999).

The amended claims are directed to a process of analyzing sequence orientation. In contrast, Ma et al. apply Bayesian neural network to recognize promoters in DNA. It does not teach the determination of the orientation of a biological sequence.

Because Ma et al does not teach every limitation of the rejected claims, Applicants respectfully request that the rejection of Claims 1, 2 and dependent Claim 3, Claims 17, 18 and dependent Claim 19 under 35 U.S.C 102 § (b) be withdrawn.

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E. Claim rejection under 35 U.S.C. § 103 should be withdrawn

Claims 1-8 and 17-24 are rejected under 35 U.S.C. § 103 (a) as being

unpatentable over Ma et al. (1999), in view of Bailey et al. (1998). Applicants

respectfully disagree with the Office Action.

The rejected claims are directed to a process of determining sequence orientation

using a Bayesian analysis of evidence (including sequence annotation) about sequence

orientation. This approach of integrating multiple sources of information for analyzing

sequence orientation is not a simple sequence search analysis. For example, the claimed

method is used to integrated annotation information.

As pointed out by the Examiner, Ma et al. does not teach analyzing sequence

orientation. However, the Examiner alleges that Ma *et al.* motivates one to use Bayesian

approach for determining characteristics for any biological sequence schemes. Ma *et al.*

discusses the use of Bayesian Neural Networks for analyzing DNA sequence

(classification). It does not teach or suggest that this approach discussed be used to

analyze orientation information, particularly annotation information. Rather, the

approach is focused on sequence analysis.

Bailey et al. was cited by the Examiner to provide motivation to applying

Bayesian approach to sequence orientation. The Examiner states that "Bailey et al. even

suggest that EST similarity searching is a practical general purpose annotation techniques

that complements pattern recognition methods as a tool for gene characterization"

However, the Examiner fails to specifically point out how Bailey *et al.* suggests or

provides motivation to the claimed method, i.e., using Bayesian analysis to integrate

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multiple sequence orientation information including sequence annotation information. While Bailey *et al.* encourages further studies in similarity based techniques and pattern recognition methods, there is no suggestion to integrate multiple sources of information via Bayesian analysis.

For the reasons above, Applicants respectfully submit that neither of the cited references disclose or suggest determination of a biological sequence's or biological sequence clusters' orientation by integrating various types of information including sequence annotation information. Therefore, this rejection of Claims 1-8 and 17-24 under 35 U.S.C. § 103 (a) should be withdrawn.

CONCLUSION

For these reasons, Applicants believe all pending claims are now in condition for allowance. If the Examiner has any questions pertaining to this application or feels that a telephone conference would in any way expedite the prosecution of the application, please do not hesitate to call the undersigned at (408) 731-5000.

The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account 01-0431.

Applicants respectfully request that a timely Notice of Allowance be issued in this case.

Respectfully submitted,

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